(FILE 'HOME' ENTERED AT 16:10:14 ON 17 APR 2002)

FILE 'BIOSIS, CAPLUS, SCISEARCH, LIFESCI, EMBASE' ENTERED AT 16:10:57 ON 17 APR 2002

L1 292 S BIOTIN SYNTHASE
L2 0 S L1 (A) MAIZE
L3 0 S L1 (A) ZEA MAYS
L4 124 DUPLICATE REMOVE L1 REMOVAL (168 DUPLICATES REMOVED)
L5 32 S L1 AND PLANT
L6 4 S L5 (A) CORN
L7 0 S L1 (A) CORN
L8 4 DUPLICATE REMOVE L6 REMOVAL (0 DUPLICATES REMOVED)

FILE 'USPATFULL, EUROPATFULL, JAPIO, PATOSWO' ENTERED AT 16:22:23 ON 17 APR 2002

L9 6 S L5

L6 ANSWER 1 OF 4 CAPLUS COPYRIGHT 2002 ACS
AN 2001:817227 CAPLUS
DN 135:368546
TI Cloning, sequences and recombinant expression of **plant** biotin synthases
IN Allen, Stephen M.; Kinney, Anthony J.; Miao, Guo-hua; Orozco, Emil M.
PA USA
SO U.S. Pat. Appl. Publ., 46 pp.
CODEN: USXXCO
DT Patent
LA English
IC ICM C12N009-00
ICS C07H021-04; C12N015-82; C12N005-04
NCL 435183000
CC 7-5 (Enzymes)
Section cross-reference(s): 3, 5, 11
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI US 2001039042	A1	20011108	US 2000-740288	20001219
PRAI US 1999-172929P	P	19991221		

AB This invention relates to an isolated nucleic acid fragment encoding a biotin synthases. Amino acid and encoding cDNA sequences of biotin synthases from barley, maize, prickly poppy, soybean and wheat are disclosed. The invention also relates to the construction of a chimeric gene encoding all or a portion of the biotin synthases, in sense or antisense orientation, wherein expression of the chimeric gene results in prodn. of altered levels of the biotin synthases in a transformed host cell.
ST **plant biotin synthase** cDNA sequence chimeric gene
IT Dicotyledon (Magnoliopsida)
Monocotyledon (Liliopsida)
(**biotin synthase** chimeric gene expression in; cloning, sequences and recombinant expression of **plant** biotin synthases)
IT Gene, **plant**
RL: AGR (Agricultural use); BPN (Biosynthetic preparation); BPR (Biological process); BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study);
PREP (Preparation); PROC (Process); USES (Uses)
(chimeric; cloning, sequences and recombinant expression of **plant** biotin synthases)
IT Bacteria (Eubacteria)
Plant cell
Yeast
(cloning host; cloning, sequences and recombinant expression of **plant** biotin synthases)
IT Argemone mexicana
Barley
Corn
Molecular cloning
Protein sequences
Soybean (Glycine max)
Transformation, genetic
Wheat
cDNA sequences
(cloning, sequences and recombinant expression of **plant**

biotin synthases)
IT Chimeric gene
RL: AGR (Agricultural use); BPN (Biosynthetic preparation); BPR (Biological process); BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study);
PREP (Preparation); PROC (Process); USES (Uses)
(**plant**; cloning, sequences and recombinant expression of **plant** biotin synthases)
IT Transgene
RL: AGR (Agricultural use); BPN (Biosynthetic preparation); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study);
PREP (Preparation); USES (Uses)
(**plant**; cloning, sequences and recombinant expression of **plant** biotin synthases)
IT Herbicides
(screening of; cloning, sequences and recombinant expression of **plant** biotin synthases)
IT **Plant** (Embryophyta)
(transgenic; cloning, sequences and recombinant expression of **plant** biotin synthases)
IT 372993-05-0DP, subfragments are claimed 372993-06-1DP, subfragments are claimed 372993-07-2DP, subfragments are claimed 372993-08-3DP, subfragments are claimed 372993-09-4DP, subfragments are claimed 372993-10-7DP, subfragments are claimed 372993-11-8DP, subfragments are claimed 372993-12-9DP, subfragments are claimed 372993-13-0DP, subfragments are claimed 372993-14-1DP, subfragments are claimed 372993-15-2DP, subfragments are claimed 372993-16-3DP, subfragments are claimed 372993-17-4DP, subfragments are claimed 372993-18-5DP, subfragments are claimed 372993-19-6DP, subfragments are claimed 373384-78-2DP, subfragments are claimed
RL: AGR (Agricultural use); BPN (Biosynthetic preparation); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study);
PREP (Preparation); USES (Uses)
(amino acid sequence; cloning, sequences and recombinant expression of **plant** biotin synthases)
IT 80146-93-6P, **Biotin synthase**
RL: AGR (Agricultural use); BPN (Biosynthetic preparation); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study);
PREP (Preparation); USES (Uses)
(cloning, sequences and recombinant expression of **plant** biotin synthases)
IT 372992-89-7DP, subfragments are claimed
RL: BPN (Biosynthetic preparation); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); PREP (Preparation); USES (Uses)
(nucleotide sequence; cloning, sequences and recombinant expression of **plant** biotin synthases)
IT 372992-90-0D, subfragments are claimed 372992-91-1D, subfragments are claimed 372992-92-2D, subfragments are claimed 372992-93-3D, subfragments are claimed 372992-94-4D, subfragments are claimed 372992-95-5D, subfragments are claimed 372992-96-6D, subfragments are claimed 372992-97-7D, subfragments are claimed 372992-98-8D, subfragments are claimed 372992-99-9D, subfragments are claimed 372993-00-5D, subfragments are claimed 372993-01-6D, subfragments are claimed 372993-02-7D, subfragments are claimed 372993-03-8D, subfragments are claimed 372993-04-9D, subfragments are claimed

RL: BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
(nucleotide sequence; cloning, sequences and recombinant expression of **plant** biotin synthases)

IT 253862-81-6 372994-37-1 373384-02-2
RL: PRP (Properties)
(unclaimed protein sequence; cloning, sequences and recombinant expression of **plant** biotin synthases)

IT 372994-38-2 372994-39-3
RL: PRP (Properties)
(unclaimed sequence; cloning, sequences and recombinant expression of **plant** biotin synthases)

L6 ANSWER 2 OF 4 CAPLUS COPYRIGHT 2002 ACS
AN 1999:104560 CAPLUS
DN 130:163980
TI Transgenic plants having increased biotin content
IN Patton, David A.
PA Novartis Finance Corporation, USA
SO U.S., 34 pp., Cont.-in-part of U.S. Ser. No. 401,068.
CODEN: USXXAM
DT Patent
LA English
IC ICM A01H005-00
ICS C12N005-04
NCL 800278000
CC 3-2 (Biochemical Genetics)
Section cross-reference(s): 11, 18
FAN.CNT 3

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	US 5869719	A	19990209	US 1997-846338	19970430
	US 5859335	A	19990112	US 1995-401068	19950308
PRAI	US 1995-401068		19950308		
	US 1994-351970		19941208		

AB The invention reveals that biotin biosynthesis in a **plant** is enhanced when the level of one or more of the enzymes in the **plant** biotin biosynthetic pathway is increased. The nutritional value of plants as dietary sources of biotin is enhanced with this invention. Provided are methods of enhancing biotin levels by introducing into **plant** tissue a chimeric gene capable of expressing a biotin biosynthetic enzyme such as **biotin synthase** or DAP aminotransferase.

ST biotin biosynthesis nutrition chimeric **plant**; synthase biotin chimeric **plant**; diaminopelargonate aminotransferase chimeric **plant**

IT Bacteria (Eubacteria)
(biotin biosynthetic enzyme from; transgenic plants having increased biotin content)

IT Escherichia coli
(biotin biosynthetic enzymes from; transgenic plants having increased biotin content)

IT Enzymes, biological studies
RL: AGR (Agricultural use); BAC (Biological activity or effector, except adverse); BPN (Biosynthetic preparation); BIOL (Biological study); PREP (Preparation); USES (Uses)
(biotin biosynthetic; transgenic plants having increased biotin content)

IT Genes (**plant**)

RL: AGR (Agricultural use); BPN (Biosynthetic preparation); BUU (Biological use, unclassified); BIOL (Biological study); PREP (Preparation); USES (Uses)
(chimeric, encoding biotin biosynthetic enzymes; transgenic plants having increased biotin content)

IT Nutrition (animal)
(enhancement of in humans; transgenic plants having increased biotin content)

IT Arabidopsis thaliana
Canola
Corn
Soybean (Glycine max)
Tobacco
Wheat
(transgenic plants having increased biotin content)

IT **Plant** (Embryophyta)
Plant cells
Plant tissue
(transgenic; transgenic plants having increased biotin content)

IT Chloroplast
(transit peptide signal sequence from; transgenic plants having increased biotin content)

IT 37259-71-5P 80146-93-6P, **Biotin synthase**
RL: AGR (Agricultural use); BAC (Biological activity or effector, except adverse); BPN (Biosynthetic preparation); BIOL (Biological study); PREP (Preparation); USES (Uses)
(biotin biosynthetic; transgenic plants having increased biotin content)

IT 9075-61-0P, 7-Keto-8-aminopelargonic acid synthetase 37259-75-9P, Desthiobiotin synthetase 55467-50-0P, Synthetase, pimelyl coenzyme a
RL: AGR (Agricultural use); BAC (Biological activity or effector, except adverse); BPN (Biosynthetic preparation); BIOL (Biological study); PREP (Preparation); USES (Uses)
(transgenic plants having increased biotin content)

IT 58-85-5P, Biotin
RL: ARG (Analytical reagent use); BPN (Biosynthetic preparation); ANST (Analytical study); BIOL (Biological study); PREP (Preparation); USES (Uses)
(transgenic plants having increased biotin content)

RE.CNT 29 THERE ARE 29 CITED REFERENCES AVAILABLE FOR THIS RECORD

RE

(1) Altschul, S; J Mol Biol 1990, V215, P403 CAPLUS
(2) Anon; GB 2216530 1989 CAPLUS
(3) Anon; EP 0635572 1994 CAPLUS
(4) Anon; WO 94/08023 1994 CAPLUS
(5) Baldet; Genbank Access No L34413 Locus ATHSEACA 1995
(6) Baldet, P; Eur J BioChem 1993, V217, P479 CAPLUS
(7) Campbell; US 5445952 1995 CAPLUS
(8) Dickson; Science 1975, V187, P27 CAPLUS
(9) Eisenberg, M; Adv Enzymol 1973, V38, P317 CAPLUS
(10) Eisenberg, M; Ann NY Acad Sci 1985, V447, P335 CAPLUS
(11) Frigg, M; Poultry Science 1983, V63, P750
(12) Gerbling; J Plant Physiol 1994, V143, P561 CAPLUS
(13) Glassman; US 5258300 1993 CAPLUS
(14) Gloeckler; US 5096823 1992 CAPLUS
(15) Gloeckler, R; Gene 1990, V87, P63 CAPLUS
(16) Knowles, J; Ann Rev BioChem 1989, V58, P195 CAPLUS
(17) Kopinski, J; British Journal of Nutrition 1989, V62, P751 CAPLUS
(18) Kopinski, J; Nutrition Reviews 1990, V48, P352
(19) Levy-Schil, S; Appl Microbiol Biotechnol 1993, V38, P755 CAPLUS

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(21) Newman, T; Plant Physiol 1994, V106, P1241 CAPLUS
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(23) Pai, C; J Bacteriol 1972, V112, P1280 CAPLUS
(24) Patton; Mol Gen Genet 1966, V251, P261
(25) Patton; Plant Physiol 1996, V112, P371 CAPLUS
(26) Robel, E; Poultry Science 1991, V70, P1716 CAPLUS
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(28) Shellhammer, A; Oklahoma State University Thesis 1986, P1
(29) Shiuan, D; Gene 1988, V67, P203 CAPLUS

L6 ANSWER 3 OF 4 CAPLUS COPYRIGHT 2002 ACS
AN 1999:48059 CAPLUS
DN 130:107731
TI Method for enhancing biotin biosynthesis in plants and transgenic plants expressing chimeric bioA or bioB genes
IN Patton, David Andrew
PA Novartis Finance Corporation, USA
SO U.S., 28 pp., Cont.-in-part of U.S. Ser. No. 351,970, abandoned.
CODEN: USXXAM
DT Patent
LA English
IC ICM A01H005-00
ICS C12N005-04; C12N015-82
NCL 800205000
CC 11-2 (Plant Biochemistry)
Section cross-reference(s): 17
FAN.CNT 3

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	US 5859335	A	19990112	US 1995-401068	19950308
	WO 9617944	A2	19960613	WO 1995-EP4659	19951127
	WO 9617944	A3	19960829		
	W: AL, AM, AU, BB, BG, BR, BY, CA, CN, CZ, EE, FI, GE, HU, IS, JP, KG, KP, KR, KZ, LK, LR, LS, LT, LV, MD, MG, MK, MN, MX, NO, NZ, PL, RO, RU, SG, SI, SK, TJ, TM, TT, UA, US, UZ, VN				
	RW: KE, LS, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
	CA 2205561	AA	19960613	CA 1995-2205561	19951127
	AU 9643001	A1	19960626	AU 1996-43001	19951127
	AU 700943	B2	19990114		
	EP 796337	A2	19970924	EP 1995-941628	19951127
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LI, LU, MC, NL, PT, SE				
	JP 10510149	T2	19981006	JP 1995-517291	19951127
	US 5869719	A	19990209	US 1997-846338	19970430
	FI 9702336	A	19970606	FI 1997-2336	19970602
PRAI	US 1994-351970		19941208		
	US 1995-401068		19950308		
	WO 1995-EP4659		19951127		

AB The present invention reveals that biotin biosynthesis in a **plant** is enhanced when the level of one or more of the enzymes in the **plant** biotin biosynthetic pathway is increased. Based upon this revelation methods which increase the level of one or more biotin biosynthetic enzymes in **plant** tissue are provided as a means for achieving enhanced levels of biotin in **plant** tissue. In particular, a method for enhancing biotin levels by introducing a chimeric gene, encoding chloroplast transit peptide fused to bacterial DAP

aminotransferase or **biotin synthase**, into **plant** tissue is provided. Resulting transgenic **plant** tissue, including whole plants, having enhanced levels of biotin is also provided. Thus, Arabidopsis expressing Escherichia coli bioA gene produced twice as much biotin as control plants. The Arabidopsis bioB was cloned and sequenced.

ST biotin prodn transgenic **plant** bioA bioB gene; sequence Arabidopsis gene bioB **biotin synthase** cDNA

IT Bacteria (Eubacteria)
Escherichia coli
(bioA or bioB genes of; method for enhancing biotin biosynthesis in plants and transgenic plants expressing chimeric bioA or bioB genes)

IT Genes (microbial)
RL: BPR (Biological process); BUU (Biological use, unclassified); BIOL (Biological study); PROC (Process); USES (Uses)
(bioA; method for enhancing biotin biosynthesis in plants and transgenic plants expressing chimeric bioA or bioB genes)

IT Genes (microbial)
RL: BPR (Biological process); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); PROC (Process); USES (Uses)
(bioB; method for enhancing biotin biosynthesis in plants and transgenic plants expressing chimeric bioA or bioB genes)

IT Chimeric genes
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(chloroplast transit peptide sequence-contg.; method for enhancing biotin biosynthesis in plants and transgenic plants expressing chimeric bioA or bioB genes)

IT cDNA sequences
(for gene bioB **biotin synthase** of Arabidopsis)

IT **Plant** cells
(method for enhancing biotin biosynthesis in plants and transgenic plants expressing chimeric bioA or bioB genes)

IT Protein sequences
(of gene bioB **biotin synthase** of Arabidopsis)

IT Arabidopsis
Canola
Corn
Plant (Embryophyta)
Soybean (Glycine max)
Tobacco
Wheat
(transgenic; method for enhancing biotin biosynthesis in plants and transgenic plants expressing chimeric bioA or bioB genes)

IT 179919-67-6
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; method for enhancing biotin biosynthesis in plants and transgenic plants expressing chimeric bioA or bioB genes)

IT 37259-71-5P 80146-93-6P, **Biotin synthase**
RL: BOC (Biological occurrence); BPN (Biosynthetic preparation); BIOL (Biological study); OCCU (Occurrence); PREP (Preparation)
(method for enhancing biotin biosynthesis in plants and transgenic plants expressing chimeric bioA or bioB genes)

IT 58-85-5, Biotin
RL: BOC (Biological occurrence); FFD (Food or feed use); MFM (Metabolic formation); BIOL (Biological study); FORM (Formation, nonpreparative); OCCU (Occurrence); USES (Uses)

(method for enhancing biotin biosynthesis in plants and transgenic plants expressing chimeric bioA or bioB genes)
IT 179919-66-5
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(nucleotide sequence; method for enhancing biotin biosynthesis in plants and transgenic plants expressing chimeric bioA or bioB genes)
RE.CNT 32 THERE ARE 32 CITED REFERENCES AVAILABLE FOR THIS RECORD
RE
(1) Altschul, S; J Mol Biol 1990, V215, P403 CAPLUS
(2) Anon; GB 2216530 1989 CAPLUS
(3) Anon; EP 0635572 A2 1994 CAPLUS
(4) Anon; WO 09408023 1994 CAPLUS
(5) Baldet; Locus ATHSEACA 1995
(6) Baldet, P; Eur J BioChem 1993, V217, P479 CAPLUS
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(11) Frigg, M; Poultry Science 1983, V63, P750
(12) Gerbling; J Plant Physiol 1994, V143, P561 CAPLUS
(13) Glassman; US 5258300 1993 CAPLUS
(14) Gloeckler; US 5096823 1992 CAPLUS
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(18) Kopinski, J; Nutrition Reviews 1990, V48, P352
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(23) Pai, C; J Bacteriol 1972, V112, P1280 CAPLUS
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(31) Wolfner, M; J Mol Biol V96, P273 CAPLUS
(32) Wu, A; Proc Natl Acad Sci U S 1978, V75, P5442 CAPLUS

L6 ANSWER 4 OF 4 CAPLUS COPYRIGHT 2002 ACS
AN 1996:494241 CAPLUS
DN 125:160360
TI Enhanced biotin formation in **plant** tissue, genetic engineering using increased enzyme formation, and transgenic **plant** as nutritional food
IN Patton, David Andrew
PA Ciba-Geigy A.-G., Switz.
SO PCT Int. Appl., 57 pp.
CODEN: PIXXD2
DT Patent
LA English
IC ICM C12N015-82
ICS C12N015-52; C12N005-10; C12N005-04; A01H005-00
CC 3-2 (Biochemical Genetics)
Section cross-reference(s): 7, 11, 17
FAN.CNT 3
PATENT NO. KIND DATE APPLICATION NO. DATE

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PI   WO 9617944        A2   19960613       WO 1995-EP4659   19951127
     WO 9617944        A3   19960829
         W:  AL, AM, AU, BB, BG, BR, BY, CA, CN, CZ, EE, FI, GE, HU, IS, JP,
             KG, KP, KR, KZ, LK, LR, LS, LT, LV, MD, MG, MK, MN, MX, NO, NZ,
             PL, RO, RU, SG, SI, SK, TJ, TM, TT, UA, US, UZ, VN
         RW: KE, LS, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FR, GB, GR, IE,
             IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR,
             NE, SN, TD, TG
     US 5859335        A    19990112       US 1995-401068   19950308
     AU 9643001        A1   19960626       AU 1996-43001    19951127
     AU 700943         B2   19990114
     EP 796337         A2   19970924       EP 1995-941628   19951127
         R:  AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LI, LU, MC, NL, PT,
SE
     JP 10510149       T2   19981006       JP 1995-517291   19951127
     FI 9702336        A    19970606       FI 1997-2336     19970602
PRAI US 1994-351970         19941208
     US 1995-401068         19950308
     WO 1995-EP4659         19951127
AB   The present invention reveals that biotin biosynthesis in a plant
     is enhanced when the level of one or more of the enzymes in the
     plant biotin biosynthetic pathway is increased.  Based upon this
     revelation methods which increase the level of one or more biotin
     biosynthetic enzymes in plant tissue are provided as a means for
     achieving enhanced levels of biotin in plant tissue.  In
     particular, a method for enhancing biotin levels by introducing a
chimeric
     gene capable of expressing a biotin biosynthetic enzyme into plant
     tissue is provided.  Resulting transgenic plant tissue,
     including whole plants, having enhanced levels of biotin are also
     provided.
ST   biotin formation genetic engineering plant enzyme
IT   Gene, plant
     RL: AGR (Agricultural use); BPR (Biological process); BUU (Biological
use,
     unclassified); PRP (Properties); BIOL (Biological study); PROC (Process);
     USES (Uses)
        (bioB; enhanced biotin formation in plant tissue, genetic
        engineering using increased enzyme formation, and transgenic
        plant as nutritional food)
IT   Arabidopsis
     Canola
       Corn
     Deoxyribonucleic acid sequences
     Genetic engineering
       Plant breeding and selection
       Plant tissue
     Protein sequences
     Soybean
     Tobacco
     Wheat
        (enhanced biotin formation in plant tissue, genetic
        engineering using increased enzyme formation, and transgenic
        plant as nutritional food)
IT   Seed
        (hybrid; enhanced biotin formation in plant tissue, genetic
        engineering using increased enzyme formation, and transgenic
        plant as nutritional food)
IT   Chloroplast
```

(targeting; enhanced biotin formation in **plant** tissue, genetic engineering using increased enzyme formation, and transgenic **plant** as nutritional food)

IT Gene, microbial
RL: AGR (Agricultural use); BPR (Biological process); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); PROC (Process); USES (Uses)
(bioA, enhanced biotin formation in **plant** tissue, genetic engineering using increased enzyme formation, and transgenic **plant** as nutritional food)

IT Gene, microbial
RL: AGR (Agricultural use); BPR (Biological process); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); PROC (Process); USES (Uses)
(bioB, enhanced biotin formation in **plant** tissue, genetic engineering using increased enzyme formation, and transgenic **plant** as nutritional food)

IT Gene, microbial
RL: AGR (Agricultural use); BPR (Biological process); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); PROC (Process); USES (Uses)
(bioC, enhanced biotin formation in **plant** tissue, genetic engineering using increased enzyme formation, and transgenic **plant** as nutritional food)

IT Gene, microbial
RL: AGR (Agricultural use); BPR (Biological process); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); PROC (Process); USES (Uses)
(bioD, enhanced biotin formation in **plant** tissue, genetic engineering using increased enzyme formation, and transgenic **plant** as nutritional food)

IT Gene, microbial
RL: AGR (Agricultural use); BPR (Biological process); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); PROC (Process); USES (Uses)
(bioF, enhanced biotin formation in **plant** tissue, genetic engineering using increased enzyme formation, and transgenic **plant** as nutritional food)

IT Gene
RL: AGR (Agricultural use); BPR (Biological process); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); PROC (Process); USES (Uses)
(chimeric, enhanced biotin formation in **plant** tissue, genetic engineering using increased enzyme formation, and transgenic **plant** as nutritional food)

IT Genetic element
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(promoter, enhanced biotin formation in **plant** tissue, genetic engineering using increased enzyme formation, and transgenic **plant** as nutritional food)

IT Genetic element
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)

(terminator, enhanced biotin formation in **plant** tissue, genetic engineering using increased enzyme formation, and transgenic **plant** as nutritional food)

IT Transformation, genetic
(transgenic, enhanced biotin formation in **plant** tissue, genetic engineering using increased enzyme formation, and transgenic **plant** as nutritional food)

IT Peptides, biological studies
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(transit, enhanced biotin formation in **plant** tissue, genetic engineering using increased enzyme formation, and transgenic **plant** as nutritional food)

IT Biological transport
(translocation, enhanced biotin formation in **plant** tissue, genetic engineering using increased enzyme formation, and transgenic **plant** as nutritional food)

IT 120861-02-1P 179919-62-1P 179919-63-2P 179919-65-4P 179919-67-6P
RL: AGR (Agricultural use); BPN (Biosynthetic preparation); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study);
PREP (Preparation); USES (Uses)
(amino acid sequence; enhanced biotin formation in **plant** tissue, genetic engineering using increased enzyme formation, and transgenic **plant** as nutritional food)

IT 120860-98-2
RL: PRP (Properties)
(amino acid sequence; enhanced biotin formation in **plant** tissue, genetic engineering using increased enzyme formation, and transgenic **plant** as nutritional food)

IT 9075-61-0P, 7-Keto-8-Aminopelargonic acid synthetase 37259-71-5P, 7,8-Diaminopelargonic acid aminotransferase 37259-75-9P, Desthiobiotin synthetase 55467-50-0P, Synthetase, pimelyl coenzyme A 80146-93-6P, **Biotin synthase**
RL: AGR (Agricultural use); BPN (Biosynthetic preparation); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study);
PREP (Preparation); USES (Uses)
(enhanced biotin formation in **plant** tissue, genetic engineering using increased enzyme formation, and transgenic **plant** as nutritional food)

IT 58-85-5P, Biotin
RL: BOC (Biological occurrence); BPN (Biosynthetic preparation); FFD (Food or feed use); BIOL (Biological study); OCCU (Occurrence); PREP (Preparation); USES (Uses)
(enhanced biotin formation in **plant** tissue, genetic engineering using increased enzyme formation, and transgenic **plant** as nutritional food)

IT 533-48-2, Desthiobiotin
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(enzyme converting desthiobiotin to 9-mercaptodesthiobiotin; enhanced biotin formation in **plant** tissue, genetic engineering using increased enzyme formation, and transgenic **plant** as nutritional food)

IT 179919-58-5 179919-61-0 179919-64-3 179919-66-5
RL: AGR (Agricultural use); BPR (Biological process); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); PROC (Process); USES (Uses)

(nucleotide sequence; enhanced biotin formation in **plant** tissue, genetic engineering using increased enzyme formation, and transgenic **plant** as nutritional food)

IT 120859-43-0, Deoxyribonucleic acid (Escherichia coli gene bioD) 179919-59-6
RL: PRP (Properties)
(nucleotide sequence; enhanced biotin formation in **plant** tissue, genetic engineering using increased enzyme formation, and transgenic **plant** as nutritional food)

> d L9 bib

L9 ANSWER 1 OF 6 USPATFULL
AN 2002:38558 USPATFULL
TI Expressed sequences of arabidopsis thaliana
IN Gorlach, Jorn, Durham, NC, UNITED STATES
An, Yong-Qiang, San Diego, CA, UNITED STATES
Hamilton, Carol M., Apex, NC, UNITED STATES
Price, Jennifer L., Raleigh, NC, UNITED STATES
Raines, Tracy M., Durham, NC, UNITED STATES
Yu, Yang, Martinsville, NJ, UNITED STATES
Rameaka, Joshua G., Durham, NC, UNITED STATES
Page, Amy, Durham, NC, UNITED STATES
Mathew, Abraham V., Cary, NC, UNITED STATES
Ledford, Brooke L., Holly Springs, NC, UNITED STATES
Woessner, Jeffrey P., Hillsborough, NC, UNITED STATES
Haas, William David, Durham, NC, UNITED STATES
Garcia, Carlos A., Carrboro, NC, UNITED STATES
Kricker, Maja, Pittsboro, NC, UNITED STATES
Slater, Ted, Apex, NC, UNITED STATES
Davis, Keith R., Durham, NC, UNITED STATES
Allen, Keith, Cary, NC, UNITED STATES
Hoffman, Neil, Chapel Hill, NC, UNITED STATES
Hurban, Patrick, Raleigh, NC, UNITED STATES
PI US 2002023280 A1 20020221
AI US 2001-770444 A1 20010126 (9)
PRAI US 2000-178502P 20000127 (60)
DT Utility
FS APPLICATION
LREP PARADIGM GENETICS, INC, 104 ALEXANDER DRIVE, BUILDING 2, P O BOX 14528, RTP, NC, 277094528
CLMN Number of Claims: 27
ECL Exemplary Claim: 1
DRWN No Drawings
LN.CNT 3845
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> d l9 2 bib

L9 ANSWER 2 OF 6 USPATFULL
AN 2001:199938 USPATFULL
TI **Plant biotin synthase**
IN Allen, Stephen M., Wilmington, DE, United States
Kinney, Anthony J., Wilmington, DE, United States
Miao, Guo-Hua, Johnston, IA, United States
Orozco, Emil M., JR., West Grove, PA, United States
PI US 2001039042 A1 20011108
AI US 2000-740288 A1 20001219 (9)
PRAI US 1999-172929P 19991221 (60)
DT Utility
FS APPLICATION
LREP E I DU PONT DE NEMOURS AND COMPANY, LEGAL DEPARTMENT - PATENTS, 1007 MARKET STREET, WILMINGTON, DE, 19898
CLMN Number of Claims: 23
ECL Exemplary Claim: 1
DRWN 3 Drawing Page(s)
LN.CNT 2682
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> d l9 3 bib

L9 ANSWER 3 OF 6 USPATFULL
AN 2001:136414 USPATFULL
TI Method to produce biotin
IN Eddy, Christina K., Loveland, CO, United States
PA BASF Aktiengesellschaft, Ludwigshafen, Germany, Federal Republic of (non-U.S. corporation)
PI US 6277609 B1 20010821
AI US 1993-1063 19930106 (8)
DT Utility
FS GRANTED
EXNAM Primary Examiner: Achutamurthy, Ponnathapu; Assistant Examiner: Moore, William W.
LREP Whyte Hirschboeck Dudek SC
CLMN Number of Claims: 24
ECL Exemplary Claim: 1
DRWN 23 Drawing Figure(s); 23 Drawing Page(s)
LN.CNT 2254
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> d l9 4 bib

L9 ANSWER 4 OF 6 USPATFULL
AN 1999:19377 USPATFULL
TI Transgenic plants having increased biotin content
IN Patton, David A., Durham, NC, United States
PA Novartis Finance Corporation, New York, NY, United States (U.S. corporation)
PI US 5869719 19990209
AI US 1997-846338 19970430 (8)
RLI Continuation-in-part of Ser. No. US 1995-401068, filed on 8 Mar 1995, now patented, Pat. No. US 5859335
DT Utility
FS Granted
EXNAM Primary Examiner: Robsinson, Douglas W.; Assistant Examiner: Zaghmout, Ousama M-Faiz
LREP Meigs, J. Timothy
CLMN Number of Claims: 13
ECL Exemplary Claim: 1
DRWN 4 Drawing Figure(s); 4 Drawing Page(s)
LN.CNT 1810
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> d l9 5 bib

L9 ANSWER 5 OF 6 USPATFULL
AN 1999:4985 USPATFULL
TI Enhanced biotin biosynthesis in **plant** tissue
IN Patton, David Andrew, Durham, NC, United States
PA Novartis Finance Corporation, New York, NY, United States (U.S. corporation)
PI US 5859335 19990112
AI US 1995-401068 19950308 (8)
RLI Continuation-in-part of Ser. No. US 1994-351970, filed on 8 Dec 1994, now abandoned
DT Utility

FS Granted
EXNAM Primary Examiner: McElwain, Elizabeth F.
LREP Meigs, J. Timothy
CLMN Number of Claims: 16
ECL Exemplary Claim: 3
DRWN 2 Drawing Figure(s); 2 Drawing Page(s)
LN.CNT 1643
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> d l9 6 bib

L9 ANSWER 6 OF 6 EUROPATFULL COPYRIGHT 2002 WILA

PATENT APPLICATION - PATENTANMELDUNG - DEMANDE DE BREVET

AN 1130094 EUROPATFULL ED 20010917 EW 200136 FS OS
TIEN Primers for synthesizing full length cDNA clones and their use.
TIDE Primer zur Synthese von vollstaendigen cDNA Klonen und ihre Verwendung.
TIFR Amorces pour la synthese de cADN de pleine longueur et leur utilisation.
IN Ota, Toshio, 1-2-7-105, Tsujido Shinmachi, Fujisawa-shi, Kanagawa 251-0042, JP;
Nishikawa, Tetsuo, 27-3-403, Hikawa-cho, Itabashi-ku, Tokyo 173-0013, JP;
Isogai, Takao, 511-12, Ohmuro, Ami-machi, Inashiki-gun, Ibaraki 300-0303, JP;
Hayashi, Koji, 1-9-446, Yushudai Nishi, Ichihara-shi, Chiba 299-0125, JP;
Ishii, Shizuko, 4508-19-202, Yana, Kisarazu-shi, Chiba 292-0812, JP;
Kawai, Yuri, 4508-19-201, Yana, Kisarazu-shi, Chiba 292-0812, JP;
Wakamatsu, Ai, 1473-4-202, Takayanagi, Kisarazu-shi, Chiba 292-0014, JP;
Sugiyama, Tomoyasu, 2-6-23-102, Kiyomidai, Kisarazu-shi, Chiba 292-0045, JP;
Nagai, Keiichi, 3-44-14-9-204, Sakuragaoka, Higashiyamato-shi, Tokyo 207-0022, JP;
Kojima, Shinichi, 2-7-10-202, Gion, Kisarazu-shi, Chiba 292-0052, JP;
Otsuki, Tetsuji, 3-1-10-B102, Asahi, Kisarazu-shi, Chiba 292-0055, JP;
Koga, Hisashi, 2-4-15, Asahi, Kisarazu-shi, Chiba 292-0055, JP
PA Helix Research Institute, 1532-3 Yana, Kisarazu-shi, Chiba 292-0812, JP
PAN 2656450
AG VOSSIUS & PARTNER, Siebertstrasse 4, 81675 Muenchen, DE
AGN 100314
OS BEPA2001070 EP 1130094 A2 1381
SO Wila-EPZ-2001-H36-T1a
DT Patent
LA Anmeldung in Englisch; Veroeffentlichung in Englisch
DS R AT; R BE; R CH; R CY; R DE; R DK; R ES; R FI; R FR; R GB; R GR; R IE; R IT; R LI; R LU; R MC; R NL; R PT; R SE; R AL; R LT; R LV; R MK; R RO; R SI
PIT EPA2 EUROPAEISCHE PATENTANMELDUNG
PI EP 1130094 A2 20010905
OD 20010905
AI EP 2000-114089 20000707
PRAI JP 1999-1944861999 19990708
JP 2000-2000118774 20000111
JP 2000-2000183765 20000502

GenCore version 4.5

OM protein - protein search, using sw model

Run on: April 17, 2002, 08:56:50 ; Search time 16.97 Seconds
(without alignments)
814.534 Million cell updates/sec

Title: US-09-740-288A-22
Perfect score: 2206
Sequence: 1 MALMLLARNLRSRLRPPLAA.....EEVSAAAPAESERSEQAASM 377

Scoring table: PAM270
Gapop 10.0 , Gapext 0.0

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1979	89.7	378	1	BIOB_ARATH	P54967 arabidopsis
2	1369	62.1	363	1	BIOB_SCHPO	O59778 schizosacch
3	1253	56.8	346	1	BIOB_ECOLI	P12996 escherichia
4	1247	56.5	346	1	BIOB_ERWHE	Q47862 erwinia her
5	1237	56.1	346	1	BIOB_SERMA	P36569 serratia ma
6	1228	55.7	375	1	BIOB_YEAST	P32451 saccharomyc
7	1184	53.7	343	1	BIOB_BUCAI	P57378 buchnera ap
8	1154	52.3	333	1	BIOB_HAEIN	P44987 haemophilus
9	1102	50.0	341	1	BIOB_METSK	P94966 methylobaci
10	863	39.1	6359	1	BACC_BACLI	O68008 b bacitraci
11	852	38.6	4568	1	DYHB_CHLRE	Q39565 chlamydomon
12	850	38.5	4644	1	DYHC_MOUSE	Q9jhu4 mus musculu
13	847	38.4	4644	1	DYHC_RAT	P38650 rattus norv
14	847	38.4	6486	1	TYCC_BACBR	O30409 b tyrocidin
15	843	38.2	4486	1	DYH9_HUMAN	Q9nyc9 homo sapien
16	840	38.1	4969	1	RYNC_RABIT	P30957 oryctolagus
17	839	38.0	4367	1	DYHC_NEUCR	P45443 neurospora
18	836	37.9	5065	1	EPPL_HUMAN	P58107 homo sapien
19	834	37.8	4540	1	DYHC_PARTE	Q27171 paramecium
20	834	37.8	5037	1	RYNR_RABIT	P11716 oryctolagus
21	829	37.6	5035	1	RYNR_PIG	P16960 sus scrofa
22	827	37.5	3530	1	MY15_HUMAN	Q9ukn7 homo sapien
23	827	37.5	4725	1	DYHC_DICDI	P34036 dictyosteli
24	826	37.4	5032	1	RYNR_HUMAN	P21817 homo sapien
25	825	37.4	4349	1	DYHC_FUSSO	P78716 fusarium so
26	823	37.3	4427	1	PKSL_BACSU	Q05470 bacillus su
27	823	37.3	5255	1	BACA_BACLI	O68006 b bacitraci
28	817	37.0	4485	1	DYHG_CHLRE	Q39575 chlamydomon
29	816	37.0	4128	1	PRKD_HUMAN	P78527 homo sapien
30	816	37.0	4466	1	DYHC_ANTCR	P39057 anthocidari
31	816	37.0	4639	1	DYHC_DROME	P37276 drosophila
32	814	36.9	4036	1	RRPL_DUGBV	Q66431 dugbe virus
33	814	36.9	4568	1	DYHC_CAEEL	Q19020 caenorhabdi
34	814	36.9	4684	1	PLE1_HUMAN	Q15149 homo sapien
35	813	36.9	4447	1	PKSK_BACSU	P40803 bacillus su
36	810	36.7	362	1	BIOB_SYNY3	P73538 synechocyst
37	808	36.6	3511	1	MY15_MOUSE	Q9qzz4 mus musculu
38	808	36.6	4544	1	LRP1_HUMAN	Q07954 homo sapien
39	807	36.6	4829	1	BIR6_HUMAN	Q9nr09 homo sapien
40	807	36.6	5217	1	HTS1_COCCA	Q01886 cochliobolu
41	806	36.5	4466	1	DYHC_TRIGR	P23098 tripneustes
42	805	36.5	4393	1	PGBM_HUMAN	P98160 homo sapien
43	805	36.5	4753	1	LRP_CAEEL	Q04833 caenorhabdi
44	803	36.4	4273	1	PKSM_BACSU	P40872 bacillus su
45	803	36.4	4344	1	DYHC_EMENI	P45444 emericella

ALIGNMENTS

RESULT 1
BIOB_ARATH
ID BIOB_ARATH STANDARD; PRT; 378 AA.
AC P54967;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE BIOTIN SYNTHASE (EC 2.8.1.6) (BIOTIN SYNTHETASE).
GN BIO2 OR BIOB OR AT2G43360 OR T01O24.10.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. LANDSBERG ERECTA;
RX MEDLINE=96417082; PubMed=8819873;
RA Weaver L.M., Yu F., Wurtele E.S., Nikolau B.J.;
RT "Characterization of the cDNA and gene coding for the biotin synthase
RT of Arabidopsis thaliana.";
RL Plant Physiol. 110:1021-1028(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA; TISSUE=Leaf;
RA Patton D., Pacella M., Ward E.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA; TISSUE=Leaf;
RX MEDLINE=96307524; PubMed=8680961;
RA Baldet P., Ruffet M.L.;
RT "Biotin synthesis in higher plants: isolation of a cDNA encoding
RT Arabidopsis thaliana bioB-gene product equivalent by functional
RT complementation of a biotin auxotroph mutant bioB105 of Escherichia
RT coli K12.";
RL C. R. Acad. Sci., III, Sci. Vie 319:99-106(1996).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
RA Moffat K.S., Cronin L.A., Shen M., VanAken S.E., Umayam L.,
RA Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
RA Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
RA Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
RA Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RT thaliana.";
RL Nature 402:761-768(1999).
CC -!- CATALYTIC ACTIVITY: DETHIOBIOTIN + (S) = BIOTIN.
CC -!- PATHWAY: LAST STEP IN BIOTIN BIOSYNTHESIS PATHWAY.
CC -!- SIMILARITY: BELONGS TO THE BIOTIN AND LIPOIC ACID SYNTHETASES
CC FAMILY.

```
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CC   ----------------------------------------------------------------------
DR   EMBL; U24147; AAA80226.1; -.
DR   EMBL; U31806; AAC49445.1; -.
DR   EMBL; L34413; AAB39953.1; -.
DR   EMBL; AC002335; AAB64312.1; -.
DR   InterPro; IPR002684; Biotin_synth.
DR   Pfam; PF01792; Biotin_synth; 1.
KW   Biotin biosynthesis; Iron-sulfur; Transferase.
FT   METAL        94     94       IRON-SULFUR (POTENTIAL).
FT   METAL        98     98       IRON-SULFUR (POTENTIAL).
FT   METAL       101    101       IRON-SULFUR (POTENTIAL).
SQ   SEQUENCE   378 AA;  41681 MW;  B102E477E7353762 CRC64;


  Query Match           89.7%;  Score 1979;  DB 1;  Length 378;
  Best Local Similarity   80.8%;  Pred. No. 5.9e-38;
  Matches  308;  Conservative   49;  Mismatches   10;  Indels   14;  Gaps    3;

Qy       4 MLLARN-LRSRLRPPLAAA-------AAFSSAAAEAERAIRDGPRNDWSRPEIQAVYDSP 55
           |:| |: :||:|||:::::       :::|:|:|||||:||:|||||||| ||::|||||
Db       1 MMLVRSVFRSQLRPSVSGGLQSASCYSSLSAASAEAERTIREGPRNDWSRDEIKSVYDSP 60

Qy      56 LLDLLFHGAQVHRNVHKFREVQQCTLLSIKTGGCSEDCSYCPQSSRYNTGLKAQKLMNKD 115
           |||||||||||||:||:|||||||||||||||||||||||||||||:||:|||:||:||
Db      61 LLDLLFHGAQVHRHVHNFREVQQCTLLSIKTGGCSEDCSYCPQSSRYSTGVKAQRLMSKD 120

Qy     116 AVLEAAKKAKESGSTRFCMGAAWRETIGRKSNFNQILEYVKEIRGMGMEVCCTLGMIEKQ 175
           ||::|||||||:|||||||||||:|||||:||:|||||:||||||||||||||||||||
Db     121 AVIDAAKKAKEAGSTRFCMGAAWRDTIGRKTNFSQILEYIKEIRGMGMEVCCTLGMIEKQ 180

Qy     176 QAEELKKAGLTAYNHNLDTSREYYPNIITTRSYDDRLQTLEHVREAGISICSGGIIGLGE 235
           || ||||||||||||||||||||||:||||||||||:|| |||:|||::|||||||||||
Db     181 QALELKKAGLTAYNHNLDTSREYYPNVITTRSYDDRLETLSHVRDAGINVCSGGIIGLGE 240

Qy     236 AEEDRVGLLHTLATLPTHPESVPINALVAVKGTPLEDQKPVEIWEMIRMIATARITMPKA 295
           |||||:||||||||||:||||||||||:||||||||||||||||||||:|||| ||||
Db     241 AEEDRIGLLHTLATLPSHPESVPINALLAVKGTPLEDQKPVEIWEMIRMIGTARIVMPKA 300

Qy     296 MVRLSAGRVRFSMPEQALCFLAGANSIFAGEKLLTTANNDFDADQAMFKILGLIPKAPSF 355
           ||||||||||||:||||||||||||:|||||||:|||||||| ||| ||||||:|||
Db     301 MVRLSAGRVRFSMSEQALCFLAGANSIFTGEKLLTTPNNDFDADQLMFKTLGLIPKPPSF 360

Qy     356 GEEEVSAAAPAESERSEQAAS 376
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Db     361 SEDD------SESENCEKVAS 375


RESULT   2
BIOB_SCHPO
ID   BIOB_SCHPO     STANDARD;      PRT;   363 AA.
AC   O59778; O60050;
DT   20-AUG-2001 (Rel. 40, Created)
DT   20-AUG-2001 (Rel. 40, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   BIOTIN SYNTHASE (EC 2.8.1.6) (BIOTIN SYNTHETASE).
GN   BIO2 OR SPCC320.01C OR SPCC1235.02.
OS   Schizosaccharomyces pombe (Fission yeast).
OC   Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC   Schizosaccharomycetales; Schizosaccharomycetaceae;
OC   Schizosaccharomyces.
OX   NCBI_TaxID=4896;
RN   [1]
RP   SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC   STRAIN=D18;
RX   MEDLINE=99456674; PubMed=1052584;
RA   Phalip V., Jeltsch J.M., Lemoine Y.;
RT   "Cloning of Schizosaccharomyces pombe bio2 by heterologous
RT   complementation of a Saccharomyces cerevisiae mutant.";
RL   Curr. Microbiol. 39:348-350(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=972;
RA   Wood V., Rajandream M.A., Barrell B.G., Wedler H., Wambutt R.;
RL   Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=972;
RA   Wood V., Rajandream M.A., Barrell B.G., Murphy L., Harris D.;
RL   Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
CC   -!- CATALYTIC ACTIVITY: DETHIOBIOTIN + (S) = BIOTIN.
CC   -!- PATHWAY: LAST STEP IN BIOTIN BIOSYNTHESIS PATHWAY.
CC   -!- SIMILARITY: BELONGS TO THE BIOTIN AND LIPOIC ACID SYNTHETASES
CC       FAMILY.
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CC   ----------------------------------------------------------------------
DR   EMBL; AJ224930; CAA12229.1; -.
DR   EMBL; AL022245; CAA18303.1; -.
DR   EMBL; AL031764; CAA21106.1; -.
DR   InterPro; IPR002684; Biotin_synth.
DR   Pfam; PF01792; Biotin_synth; 1.
KW   Biotin biosynthesis; Iron-sulfur; Transferase.
FT   METAL        69     69       IRON-SULFUR (POTENTIAL).
FT   METAL        73     73       IRON-SULFUR (POTENTIAL).
FT   METAL        76     76       IRON-SULFUR (POTENTIAL).
FT   CONFLICT     13     14       SS -> FF (IN REF. 1).
FT   CONFLICT     17     17       S -> F (IN REF. 1).
FT   CONFLICT    312    318       TTPAVSW -> LLLLFL (IN REF. 1).
SQ   SEQUENCE   363 AA;  40650 MW;  008E2EDF9901AEB1 CRC64;


  Query Match           62.1%;  Score 1369;  DB 1;  Length 363;
  Best Local Similarity   52.8%;  Pred. No. 5.3e-23;
  Matches  204;  Conservative   81;  Mismatches   65;  Indels   36;  Gaps    6;

Qy       5 LLARNLRSRLRPPLAAAAAFSSAAAEAERAIRDGP----RNDWSRPEIQAVYDSPLLDLL 60
           :::|::| ::|                    | ::    ||:|:| ||| :||:||:||:
Db       1 MFTRTIRQQIR-------------------RSSALSLVRNNWTREEIQKIYDTPLIDLI 40

Qy      61 FHGAQVHRNVHKFREVQQCTLLSIKTGGCSEDCSYCPQSSRYNTGLKAQKLMNKDAVLEA 120
           |::| :||: |  : ||||||||||||||:||| ||:||||||||:|| ||||: | |||
Db      41 FRAASIHRKFHDPKKVQQCTLLSIKTGGCTEDCKYCAQSSRYNTGVKATKLMKIDEVLEK 100

Qy     121 AKKAKESGSTRFCMGAAWRETIGRKSNFNQILEYVKEIRGMGMEVCCTLGMIEKQQAEEL 180
           || ||  ||||||||:|||:  ||: :|::||| :||:|:|:|:|||| ||||:: ||| ||
Db     101 AKIAKAKGSTRFCMGSAWRDLNGRNRTFKNILEIIKEVRSMDMEVCVTLGMLNEQQAKEL 160

Qy     181 KKAGLTAYNHNLDTSREYYPNIITTRSYDDRLQTLEHVREAGISICSGGIIGLGEAEEDR 240
           | |||||||||||||||::||:||:||:||:|::::| ||: :|||||:|||| :||
Db     161 KDAGLTAYNHNLDTSREYYSKIISTRTYDERLNTIDNLRKAGLKVCSGGILGLGEKKHDR 220

Qy     241 VGLLHTLATLPTHPESVPINALVAVKGTPLED--QKPVEIWEMIRMIATARITMPKAMVR 298
           |||:|:|||:||||||||:| ||:: |||: |  :  : |   :| |||||| |||:::|
Db     221 VGLIHSLATMPTHPESVPFNLLVPIPGTPVGDAVKERLPIHPFLRSIATARICMPKTIIR 280

Qy     299 LSAGRVRFSMPEQALCFLAGANSIFAGEKLLTTANNDFDADQAMFKILGLIPKAPSF--- 355
           ::|||   | :|||| |:||||::|:|||:|||:   :|:|  :|   ||     ||
Db     281 FAAGRNTCSESEQALAFMAGANAVFTGEKMLTTPAVSWDSDSQLFYNWGLEGM-QSFEYG 339

Qy     356 ----GEEEVSAAAPAESERSEQAASM 377
               ||:   : :|   ||   ::|:
Db     340 TSTEGEDGTFTLPP--KERLAPSPSL 363
```

OM protein - protein search, using sw model

Run on: April 17, 2002, 08:59:13 ; Search time 16.97 Seconds
(without alignments)
814.534 Million cell updates/sec

Title: US-09-740-288A-24
Perfect score: 2212
Sequence: 1 MALMLLARNLRSRLRPPLAA.....EEASAAAPTESERSEQAASM 377

Scoring table: PAM270
Gapop 10.0 , Gapext 0.0

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1970	89.1	378	1	BIOB_ARATH	P54967 arabidopsis
2	1360	61.5	363	1	BIOB_SCHPO	O59778 schizosacch
3	1242	56.1	346	1	BIOB_ECOLI	P12996 escherichia
4	1233	55.7	346	1	BIOB_ERWHE	Q47862 erwinia her
5	1230	55.6	346	1	BIOB_SERMA	P36569 serratia ma
6	1218	55.1	375	1	BIOB_YEAST	P32451 saccharomyc
7	1175	53.1	343	1	BIOB_BUCAI	P57378 buchnera ap
8	1143	51.7	333	1	BIOB_HAEIN	P44987 haemophilus
9	1098	49.6	341	1	BIOB_METSK	P94966 methylobaci
10	862	39.0	6359	1	BACC_BACLI	O68008 b bacitraci
11	857	38.7	4568	1	DYHB_CHLRE	Q39565 chlamydomon
12	854	38.6	6486	1	TYCC_BACBR	O30409 b tyrocidin
13	847	38.3	4969	1	RYNC_RABIT	P30957 oryctolagus
14	846	38.2	4644	1	DYHC_MOUSE	Q9jhu4 mus musculu
15	845	38.2	4367	1	DYHC_NEUCR	P45443 neurospora
16	843	38.1	4644	1	DYHC_RAT	P38650 rattus norv
17	839	37.9	5037	1	RYNR_RABIT	P11716 oryctolagus
18	839	37.9	5065	1	EPPL_HUMAN	P58107 homo sapien
19	838	37.9	4427	1	PKSL_BACSU	Q05470 bacillus su
20	838	37.9	4486	1	DYH9_HUMAN	Q9nyc9 homo sapien
21	831	37.6	4725	1	DYHC_DICDI	P34036 dictyosteli
22	831	37.6	5035	1	RYNR_PIG	P16960 sus scrofa
23	831	37.6	5255	1	BACA_BACLI	O68006 b bacitraci
24	830	37.5	5032	1	RYNR_HUMAN	P21817 homo sapien
25	828	37.4	4540	1	DYHC_PARTE	Q27171 paramecium
26	824	37.3	3530	1	MY15_HUMAN	Q9ukn7 homo sapien
27	823	37.2	4349	1	DYHC_FUSSO	P78716 fusarium so
28	821	37.1	4273	1	PKSM_BACSU	P40872 bacillus su
29	821	37.1	4485	1	DYHG_CHLRE	Q39575 chlamydomon
30	817	36.9	4684	1	PLE1_HUMAN	Q15149 homo sapien
31	816	36.9	4036	1	RRPL_DUGBV	Q66431 dugbe virus
32	816	36.9	4447	1	PKSK_BACSU	P40803 bacillus su
33	815	36.8	4128	1	PRKD_HUMAN	P78527 homo sapien
34	814	36.8	4568	1	DYHC_CAEEL	Q19020 caenorhabdi
35	813	36.8	4466	1	DYHC_ANTCR	P39057 anthocidari
36	813	36.8	4543	1	LRP1_CHICK	P98157 gallus gall
37	811	36.7	362	1	BIOB_SYNY3	P73538 synechocyst
38	811	36.7	4639	1	DYHC_DROME	P37276 drosophila
39	811	36.7	5217	1	HTS1_COCCA	Q01886 cochliobolu
40	809	36.6	4544	1	LRP1_HUMAN	Q07954 homo sapien
41	809	36.6	4687	1	PLE1_RAT	P30427 rattus norv
42	808	36.5	4344	1	DYHC_EMENI	P45444 emericella
43	807	36.5	4466	1	DYHC_TRIGR	P23098 tripneustes
44	807	36.5	4753	1	LRP_CAEEL	Q04833 caenorhabdi
45	807	36.5	5327	1	ACF7_MOUSE	Q9qxz0 mus musculu

ALIGNMENTS

RESULT 1
BIOB_ARATH
ID BIOB_ARATH STANDARD; PRT; 378 AA.
AC P54967;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE BIOTIN SYNTHASE (EC 2.8.1.6) (BIOTIN SYNTHETASE).
GN BIO2 OR BIOB OR AT2G43360 OR T01O24.10.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. LANDSBERG ERECTA;
RX MEDLINE=96417082; PubMed=8819873;
RA Weaver L.M., Yu F., Wurtele E.S., Nikolau B.J.;
RT "Characterization of the cDNA and gene coding for the biotin synthase
RT of Arabidopsis thaliana.";
RL Plant Physiol. 110:1021-1028(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA; TISSUE=Leaf;
RA Patton D., Pacella M., Ward E.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA; TISSUE=Leaf;
RX MEDLINE=96307524; PubMed=8680961;
RA Baldet P., Ruffet M.L.;
RT "Biotin synthesis in higher plants: isolation of a cDNA encoding
RT Arabidopsis thaliana bioB-gene product equivalent by functional
RT complementation of a biotin auxotroph mutant bioB105 of Escherichia
RT coli K12.";
RL C. R. Acad. Sci., III, Sci. Vie 319:99-106(1996).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
RA Moffat K.S., Cronin L.A., Shen M., VanAken S.E., Umayam L.,
RA Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
RA Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
RA Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
RA Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RT thaliana.";
RL Nature 402:761-768(1999).
CC -!- CATALYTIC ACTIVITY: DETHIOBIOTIN + (S) = BIOTIN.
CC -!- PATHWAY: LAST STEP IN BIOTIN BIOSYNTHESIS PATHWAY.
CC -!- SIMILARITY: BELONGS TO THE BIOTIN AND LIPOIC ACID SYNTHETASES
CC FAMILY.

```
CC   ----------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; U24147; AAA80226.1; -.
DR   EMBL; U31806; AAC49445.1; -.
DR   EMBL; L34413; AAB39953.1; -.
DR   EMBL; AC002335; AAB64312.1; -.
DR   InterPro; IPR002684; Biotin_synth.
DR   Pfam; PF01792; Biotin_synth; 1.
KW   Biotin biosynthesis; Iron-sulfur; Transferase.
FT   METAL        94     94       IRON-SULFUR (POTENTIAL).
FT   METAL        98     98       IRON-SULFUR (POTENTIAL).
FT   METAL       101    101       IRON-SULFUR (POTENTIAL).
SQ   SEQUENCE   378 AA;  41681 MW;  B102E477E7353762 CRC64;

  Query Match             89.1%;  Score 1970;  DB 1;  Length 378;
  Best Local Similarity   80.6%;  Pred. No. 7e-37;
  Matches  307;  Conservative   49;  Mismatches   11;  Indels   14;  Gaps    3;

Qy       4 MLLARN-LRSRLRPPLAAA-------AAFSSAAAEAERAIRDGPRNDWSRPEIQAVYDSP 55
           |:| |: :||:|||:::::        :::|:|:||||:||:|||||||| ||::|||||
Db       1 MMLVRSVFRSQLRPSVSGGLQSASCYSSLSAASAEAERTIREGPRNDWSRDEIKSVYDSP 60

Qy      56 LLDLLFHGAQVHRNVHKFREVQQCTLLSIKTGGCSEDCSYCPQSSRYNTGLKAQKLMNKY 115
           ||||||||||||||:||:|||||||||||||||||||||||||||||:||:|||:||:|
Db      61 LLDLLFHGAQVHRHVHNFREVQQCTLLSIKTGGCSEDCSYCPQSSRYSTGVKAQRLMSKD 120

Qy     116 AVLEAAKKAKESGSTRFCMGAAWRETIGRKSNFNQILEYVKEIRGMGMEVCCTLGMIEKQ 175
           ||::|||||||:||||||||||||:|||||:||:|||||:|||||||||||||||||||||
Db     121 AVIDAAKKAKEAGSTRFCMGAAWRDTIGRKTNFSQILEYIKEIRGMGMEVCCTLGMIEKQ 180

Qy     176 QAEELKKAGLTAYNHNLDTSREYYPNIITTRSYDDRLQTLEHVREAGISICSGGIIGLGE 235
           || ||||||||||||||||||||||:||||||||||:|| |||:|||::||||||||||
Db     181 QALELKKAGLTAYNHNLDTSREYYPNVITTRSYDDRLETLSHVRDAGINVCSGGIIGLGE 240

Qy     236 AEEDRVGLLHTLATLPTHPESVPINALVAVKGTPLEDQKPVEIWEMIRMIATARITMPKA 295
           |||||:|||||||||||:|||||||||:|||||||||||||||||||:|||| ||||
Db     241 AEEDRIGLLHTLATLPSHPESVPINALLAVKGTPLEDQKPVEIWEMIRMIGTARIVMPKA 300

Qy     296 MVRLSAGRVRFSMPEQALCFLAGANSIFAGEKLLTTANNDFDADQAMFKILGLIPKAPSF 355
           |||||||||||:|||||||||||||:|||||||:|||||||| ||| ||||||:|||
Db     301 MVRLSAGRVRFSMSEQALCFLAGANSIFTGEKLLTTPNNDFDADQLMFKTLGLIPKPPSF 360

Qy     356 GEEEASAAAPTESERSEQAAS 376
           :|::      :|||  |: ||
Db     361 SEDD------SESENCEKVAS 375


RESULT   2
BIOB_SCHPO
ID   BIOB_SCHPO     STANDARD;      PRT;   363 AA.
AC   O59778; O60050;
DT   20-AUG-2001 (Rel. 40, Created)
DT   20-AUG-2001 (Rel. 40, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   BIOTIN SYNTHASE (EC 2.8.1.6) (BIOTIN SYNTHETASE).
GN   BIO2 OR SPCC320.01C OR SPCC1235.02.
OS   Schizosaccharomyces pombe (Fission yeast).
OC   Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC   Schizosaccharomycetales; Schizosaccharomycetaceae;
OC   Schizosaccharomyces.
OX   NCBI_TaxID=4896;
RN   [1]
RP   SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC   STRAIN=D18;
RX   MEDLINE=99456674; PubMed=1052584;
RA   Phalip V., Jeltsch J.M., Lemoine Y.;
RT   "Cloning of Schizosaccharomyces pombe bio2 by heterologous
RT   complementation of a Saccharomyces cerevisiae mutant.";
RL   Curr. Microbiol. 39:348-350(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=972;
RA   Wood V., Rajandream M.A., Barrell B.G., Wedler H., Wambutt R.;
RL   Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=972;
RA   Wood V., Rajandream M.A., Barrell B.G., Murphy L., Harris D.;
RL   Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
CC   -!- CATALYTIC ACTIVITY: DETHIOBIOTIN + (S) = BIOTIN.
CC   -!- PATHWAY: LAST STEP IN BIOTIN BIOSYNTHESIS PATHWAY.
CC   -!- SIMILARITY: BELONGS TO THE BIOTIN AND LIPOIC ACID SYNTHETASES
CC       FAMILY.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AJ224930; CAA12229.1; -.
DR   EMBL; AL022245; CAA18303.1; -.
DR   EMBL; AL031764; CAA21106.1; -.
DR   InterPro; IPR002684; Biotin_synth.
DR   Pfam; PF01792; Biotin_synth; 1.
KW   Biotin biosynthesis; Iron-sulfur; Transferase.
FT   METAL        69     69       IRON-SULFUR (POTENTIAL).
FT   METAL        73     73       IRON-SULFUR (POTENTIAL).
FT   METAL        76     76       IRON-SULFUR (POTENTIAL).
FT   CONFLICT     13     14       SS -> FF (IN REF. 1).
FT   CONFLICT     17     17       S -> F (IN REF. 1).
FT   CONFLICT    312    318       TTPAVSW -> LLLLFL (IN REF. 1).
SQ   SEQUENCE   363 AA;  40650 MW;  008E2EDF9901AEB1 CRC64;

  Query Match             61.5%;  Score 1360;  DB 1;  Length 363;
  Best Local Similarity   52.6%;  Pred. No. 3.3e-22;
  Matches  203;  Conservative   82;  Mismatches   65;  Indels   36;  Gaps    6;

Qy       5 LLARNLRSRLRPPLAAAAAFSSAAAEAERAIRDGP----RNDWSRPEIQAVYDSPLLDLL 60
           :::|::| ::|                    | ::    ||:|:| ||| :||:||:||:
Db       1 MFTRTIRQQIR--------------------RSSALSLVRNNWTREEIQKIYDTPLIDLI 40

Qy      61 FHGAQVHRNVHKFREVQQCTLLSIKTGGCSEDCSYCPQSSRYNTGLKAQKLMNKYAVLEA 120
           |::| :||: |  : ||||||||||||||:||| ||:|||||||:|| |||:   |||
Db      41 FRAASIHRKFHDPKKVQQCTLLSIKTGGCTEDCKYCAQSSRYNTGVKATKLMKIDEVLEK 100

Qy     121 AKKAKESGSTRFCMGAAWRETIGRKSNFNQILEYVKEIRGMGMEVCCTLGMIEKQQAEEL 180
           || ||  ||||||||:|||:  ||: :|::||| :||:|:|:|||| ||||:: ||| ||
Db     101 AKIAKAKGSTRFCMGSAWRDLNGRNRTFKNILEIIKEVRSMDMEVCVTLGMLNEQQAKEL 160

Qy     181 KKAGLTAYNHNLDTSREYYPNIITTRSYDDRLQTLEHVREAGISICSGGIIGLGEAEEDR 240
           | ||||||||||||||||::||:||:||:||:|::::| ||: :|||||:|||| :||
Db     161 KDAGLTAYNHNLDTSREYYSKIISTRTYDERLNTIDNLRKAGLKVCSGGILGLGEKKHDR 220

Qy     241 VGLLHTLATLPTHPESVPINALVAVKGTPLED--QKPVEIWEMIRMIATARITMPKAMVR 298
           |||:|:|||:|||||||||:| ||:: |||: |  :  : |   :| |||||| |||:::|
Db     221 VGLIHSLATMPTHPESVPFNLLVPIPGTPVGDAVKERLPIHPFLRSIATARICMPKTIIR 280

Qy     299 LSAGRVRFSMPEQALCFLAGANSIFAGEKLLTTANNDFDADQAMFKILGLIPKAPSF--- 355
           ::|||   | :|||| |:||||::|:|||:|||:   :|:|  :|   ||     ||
Db     281 FAAGRNTCSESEQALAFMAGANAVFTGEKMLTTPAVSWDSDSQLFYNWGLEGM-QSFEYG 339

Qy     356 ----GEEEASAAAPTESERSEQAASM 377
               ||: : : :|   ||   ::|:
Db     340 TSTEGEDGTFTLPP--KERLAPSPSL 363
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GenCore version 4.5

OM protein - protein search, using sw model

Run on: April 17, 2002, 08:59:13 ; Search time 16.97 Seconds
(without alignments)
814.534 Million cell updates/sec

Title: US-09-740-288A-24
Perfect score: 2212
Sequence: 1 MALMLLARNLRSRLRPPLAA.....EEASAAAPTESERSEQAASM 377

Scoring table: PAM270
Gapop 10.0 , Gapext 0.0

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	1360	61.5	363	1	BIOB_SCHPO	O59778 schizosacch
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4	1233	55.7	346	1	BIOB_ERWHE	Q47862 erwinia her
5	1230	55.6	346	1	BIOB_SERMA	P36569 serratia ma
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8	1143	51.7	333	1	BIOB_HAEIN	P44987 haemophilus
9	1098	49.6	341	1	BIOB_METSK	P94966 methylobaci
10	862	39.0	6359	1	BACC_BACLI	O68008 b bacitraci
11	857	38.7	4568	1	DYHB_CHLRE	Q39565 chlamydomon
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14	846	38.2	4644	1	DYHC_MOUSE	Q9jhu4 mus musculu
15	845	38.2	4367	1	DYHC_NEUCR	P45443 neurospora
16	843	38.1	4644	1	DYHC_RAT	P38650 rattus norv
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20	838	37.9	4486	1	DYH9_HUMAN	Q9nyc9 homo sapien
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22	831	37.6	5035	1	RYNR_PIG	P16960 sus scrofa
23	831	37.6	5255	1	BACA_BACLI	O68006 b bacitraci
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25	828	37.4	4540	1	DYHC_PARTE	Q27171 paramecium
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27	823	37.2	4349	1	DYHC_FUSSO	P78716 fusarium so
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33	815	36.8	4128	1	PRKD_HUMAN	P78527 homo sapien
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38	811	36.7	4639	1	DYHC_DROME	P37276 drosophila
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44	807	36.5	4753	1	LRP_CAEEL	Q04833 caenorhabdi
45	807	36.5	5327	1	ACF7_MOUSE	Q9qxz0 mus musculu

ALIGNMENTS

RESULT 1
BIOB_ARATH
ID BIOB_ARATH STANDARD; PRT; 378 AA.
AC P54967;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE BIOTIN SYNTHASE (EC 2.8.1.6) (BIOTIN SYNTHETASE).
GN BIO2 OR BIOB OR AT2G43360 OR T01O24.10.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. LANDSBERG ERECTA;
RX MEDLINE=96417082; PubMed=8819873;
RA Weaver L.M., Yu F., Wurtele E.S., Nikolau B.J.;
RT "Characterization of the cDNA and gene coding for the biotin synthase
RT of Arabidopsis thaliana.";
RL Plant Physiol. 110:1021-1028(1996).
RN [2]
RP SEQUENCE FROM N.A.
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RA Patton D., Pacella M., Ward E.;
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RX MEDLINE=96307524; PubMed=8680961;
RA Baldet P., Ruffet M.L.;
RT "Biotin synthesis in higher plants: isolation of a cDNA encoding
RT Arabidopsis thaliana bioB-gene product equivalent by functional
RT complementation of a biotin auxotroph mutant bioB105 of Escherichia
RT coli K12.";
RL C. R. Acad. Sci., III, Sci. Vie 319:99-106(1996).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
RA Moffat K.S., Cronin L.A., Shen M., VanAken S.E., Umayam L.,
RA Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
RA Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
RA Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
RA Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RT thaliana.";
RL Nature 402:761-768(1999).
CC -!- CATALYTIC ACTIVITY: DETHIOBIOTIN + (S) = BIOTIN.
CC -!- PATHWAY: LAST STEP IN BIOTIN BIOSYNTHESIS PATHWAY.
CC -!- SIMILARITY: BELONGS TO THE BIOTIN AND LIPOIC ACID SYNTHETASES
CC FAMILY.

```
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; U24147; AAA80226.1; -.
DR   EMBL; U31806; AAC49445.1; -.
DR   EMBL; L34413; AAB39953.1; -.
DR   EMBL; AC002335; AAB64312.1; -.
DR   InterPro; IPR002684; Biotin_synth.
DR   Pfam; PF01792; Biotin_synth; 1.
KW   Biotin biosynthesis; Iron-sulfur; Transferase.
FT   METAL        94     94       IRON-SULFUR (POTENTIAL).
FT   METAL        98     98       IRON-SULFUR (POTENTIAL).
FT   METAL       101    101       IRON-SULFUR (POTENTIAL).
SQ   SEQUENCE   378 AA;  41681 MW;  B102E477E7353762 CRC64;


  Query Match             89.1%;  Score 1970;  DB 1;  Length 378;
  Best Local Similarity   80.6%;  Pred. No. 7e-37;
  Matches  307;  Conservative   49;  Mismatches   11;  Indels   14;  Gaps    3;

Qy       4 MLLARN-LRSRLRPPLAAA-------AAFSSAAAEAERAIRDGPRNDWSRPEIQAVYDSP 55
           |:| |: :||:|||:::::       :::|:|:|||||:||:|||||||| ||::|||||
Db       1 MMLVRSVFRSQLRPSVSGGLQSASCYSSLSAASAEAERTIREGPRNDWSRDEIKSVYDSP 60

Qy      56 LLDLLFHGAQVHRNVHKFREVQQCTLLSIKTGGCSEDCSYCPQSSRYNTGLKAQKLMNKY 115
           ||||||||||||||:||:|||||||||||||||||||||||||||:||:|||:||:|
Db      61 LLDLLFHGAQVHRHVHNFREVQQCTLLSIKTGGCSEDCSYCPQSSRYSTGVKAQRLMSKD 120

Qy     116 AVLEAAKKAKESGSTRFCMGAAWRETIGRKSNFNQILEYVKEIRGMGMEVCCTLGMIEKQ 175
           ||::|||||||:|||||||||||||:|||||:||:|||||:|||||||||||||||||||
Db     121 AVIDAAKKAKEAGSTRFCMGAAWRDTIGRKTNFSQILEYIKEIRGMGMEVCCTLGMIEKQ 180

Qy     176 QAEELKKAGLTAYNHNLDTSREYYPNIITTRSYDDRLQTLEHVREAGISICSGGIIGLGE 235
           || |||||||||||||||||||||||:|||||||||:|| |||:|||::|||||||||||
Db     181 QALELKKAGLTAYNHNLDTSREYYPNVITTRSYDDRLETLSHVRDAGINVCSGGIIGLGE 240

Qy     236 AEEDRVGLLHTLATLPTHPESVPINALVAVKGTPLEDQKPVEIWEMIRMIATARITMPKA 295
           |||||:||||||||||:||||||||||:|||||||||||||||||||:|||| ||||
Db     241 AEEDRIGLLHTLATLPSHPESVPINALLAVKGTPLEDQKPVEIWEMIRMIGTARIVMPKA 300

Qy     296 MVRLSAGRVRFSMPEQALCFLAGANSIFAGEKLLTTANNDFDADQAMFKILGLIPKAPSF 355
           |||||||||||||:|||||||||||||:|||||||:|||||||| ||| ||||||:|||
Db     301 MVRLSAGRVRFSMSEQALCFLAGANSIFTGEKLLTTPNNDFDADQLMFKTLGLIPKPPSF 360

Qy     356 GEEEASAAAPTESERSEQAAS 376
           :|::      :|||  |: ||
Db     361 SEDD------SESENCEKVAS 375


RESULT   2
BIOB_SCHPO
ID   BIOB_SCHPO     STANDARD;      PRT;   363 AA.
AC   O59778; O60050;
DT   20-AUG-2001 (Rel. 40, Created)
DT   20-AUG-2001 (Rel. 40, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   BIOTIN SYNTHASE (EC 2.8.1.6) (BIOTIN SYNTHETASE).
GN   BIO2 OR SPCC320.01C OR SPCC1235.02.
OS   Schizosaccharomyces pombe (Fission yeast).
OC   Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC   Schizosaccharomycetales; Schizosaccharomycetaceae;
OC   Schizosaccharomyces.
OX   NCBI_TaxID=4896;
RN   [1]
RP   SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC   STRAIN=D18;
RX   MEDLINE=99456674; PubMed=1052584;
RA   Phalip V., Jeltsch J.M., Lemoine Y.;
RT   "Cloning of Schizosaccharomyces pombe bio2 by heterologous
RT   complementation of a Saccharomyces cerevisiae mutant.";
RL   Curr. Microbiol. 39:348-350(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=972;
RA   Wood V., Rajandream M.A., Barrell B.G., Wedler H., Wambutt R.;
RL   Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=972;
RA   Wood V., Rajandream M.A., Barrell B.G., Murphy L., Harris D.;
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CC   -!- CATALYTIC ACTIVITY: DETHIOBIOTIN + (S) = BIOTIN.
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CC       FAMILY.
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AJ224930; CAA12229.1; -.
DR   EMBL; AL022245; CAA18303.1; -.
DR   EMBL; AL031764; CAA21106.1; -.
DR   InterPro; IPR002684; Biotin_synth.
DR   Pfam; PF01792; Biotin_synth; 1.
KW   Biotin biosynthesis; Iron-sulfur; Transferase.
FT   METAL        69     69       IRON-SULFUR (POTENTIAL).
FT   METAL        73     73       IRON-SULFUR (POTENTIAL).
FT   METAL        76     76       IRON-SULFUR (POTENTIAL).
FT   CONFLICT     13     14       SS -> FF (IN REF. 1).
FT   CONFLICT     17     17       S -> F (IN REF. 1).
FT   CONFLICT    312    318       TTPAVSW -> LLLLFL (IN REF. 1).
SQ   SEQUENCE   363 AA;  40650 MW;  008E2EDF9901AEB1 CRC64;


  Query Match             61.5%;  Score 1360;  DB 1;  Length 363;
  Best Local Similarity   52.6%;  Pred. No. 3.3e-22;
  Matches  203;  Conservative   82;  Mismatches   65;  Indels   36;  Gaps    6;

Qy       5 LLARNLRSRLRPPLAAAAAFSSAAAEAERAIRDGP----RNDWSRPEIQAVYDSPLLDLL 60
           :::|::| ::|                  | ::    ||:|:| ||| :||:||:||:
Db       1 MFTRTIRQQIR------------------RSSALSLVRNNWTREEIQKIYDTPLIDLI 40

Qy      61 FHGAQVHRNVHKFREVQQCTLLSIKTGGCSEDCSYCPQSSRYNTGLKAQKLMNKYAVLEA 120
           |::| :||: |  : |||||||||||||:||| ||:||||||||:|| |||:   |||
Db      41 FRAASIHRKFHDPKKVQQCTLLSIKTGGCTEDCKYCAQSSRYNTGVKATKLMKIDEVLEK 100

Qy     121 AKKAKESGSTRFCMGAAWRETIGRKSNFNQILEYVKEIRGMGMEVCCTLGMIEKQQAEEL 180
           || ||  ||||||||:|||:  ||: :|::||| :||:|:|:|||| ||||:: ||| ||
Db     101 AKIAKAKGSTRFCMGSAWRDLNGRNRTFKNILEIIKEVRSMDMEVCVTLGMLNEQQAKEL 160

Qy     181 KKAGLTAYNHNLDTSREYYPNIITTRSYDDRLQTLEHVREAGISICSGGIIGLGEAEEDR 240
           | |||||||||||||||::||:||:||:||:|::::| ||: :|||||:|||| :||
Db     161 KDAGLTAYNHNLDTSREYYSKIISTRTYDERLNTIDNLRKAGLKVCSGGILGLGEKKHDR 220

Qy     241 VGLLHTLATLPTHPESVPINALVAVKGTPLED--QKPVEIWEMIRMIATARITMPKAMVR 298
           |||:|:|||:|||||||:| ||:: |||: |  :  : |   :| |||||| |||:::|
Db     221 VGLIHSLATMPTHPESVPFNLLVPIPGTPVGDAVKERLPIHPFLRSIATARICMPKTIIR 280

Qy     299 LSAGRVRFSMPEQALCFLAGANSIFAGEKLLTTANNDFDADQAMFKILGLIPKAPSF--- 355
           ::|||   | :|||| |:||||::|:|||:|||:   :|:|  :|   ||     ||
Db     281 FAAGRNTCSESEQALAFMAGANAVFTGEKMLTTPAVSWDSDSQLFYNWGLEGM-QSFEYG 339

Qy     356 ----GEEEASAAAPTESERSEQAASM 377
               ||: : : :|   ||   ::|:
Db     340 TSTEGEDGTFTLPP--KERLAPSPSL 363
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OM protein - protein search, using sw model

Run on: April 17, 2002, 08:56:50 ; Search time 16.97 Seconds
(without alignments)
814.534 Million cell updates/sec

Title: US-09-740-288A-22
Perfect score: 2206
Sequence: 1 MALMLLARNLRSRLRPPLAA.....EEVSAAAPAESERSEQAASM 377

Scoring table: PAM270
Gapop 10.0 , Gapext 0.0

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1979	89.7	378	1	BIOB_ARATH	P54967 arabidopsis
2	1369	62.1	363	1	BIOB_SCHPO	O59778 schizosacch
3	1253	56.8	346	1	BIOB_ECOLI	P12996 escherichia
4	1247	56.5	346	1	BIOB_ERWHE	Q47862 erwinia her
5	1237	56.1	346	1	BIOB_SERMA	P36569 serratia ma
6	1228	55.7	375	1	BIOB_YEAST	P32451 saccharomyc
7	1184	53.7	343	1	BIOB_BUCAI	P57378 buchnera ap
8	1154	52.3	333	1	BIOB_HAEIN	P44987 haemophilus
9	1102	50.0	341	1	BIOB_METSK	P94966 methylobaci
10	863	39.1	6359	1	BACC_BACLI	O68008 b bacitraci
11	852	38.6	4568	1	DYHB_CHLRE	Q39565 chlamydomon
12	850	38.5	4644	1	DYHC_MOUSE	Q9jhu4 mus musculu
13	847	38.4	4644	1	DYHC_RAT	P38650 rattus norv
14	847	38.4	6486	1	TYCC_BACBR	O30409 b tyrocidin
15	843	38.2	4486	1	DYH9_HUMAN	Q9nyc9 homo sapien
16	840	38.1	4969	1	RYNC_RABIT	P30957 oryctolagus
17	839	38.0	4367	1	DYHC_NEUCR	P45443 neurospora
18	836	37.9	5065	1	EPPL_HUMAN	P58107 homo sapien
19	834	37.8	4540	1	DYHC_PARTE	Q27171 paramecium
20	834	37.8	5037	1	RYNR_RABIT	P11716 oryctolagus
21	829	37.6	5035	1	RYNR_PIG	P16960 sus scrofa
22	827	37.5	3530	1	MY15_HUMAN	Q9ukn7 homo sapien
23	827	37.5	4725	1	DYHC_DICDI	P34036 dictyosteli
24	826	37.4	5032	1	RYNR_HUMAN	P21817 homo sapien
25	825	37.4	4349	1	DYHC_FUSSO	P78716 fusarium so
26	823	37.3	4427	1	PKSL_BACSU	Q05470 bacillus su
27	823	37.3	5255	1	BACA_BACLI	O68006 b bacitraci
28	817	37.0	4485	1	DYHG_CHLRE	Q39575 chlamydomon
29	816	37.0	4128	1	PRKD_HUMAN	P78527 homo sapien
30	816	37.0	4466	1	DYHC_ANTCR	P39057 anthocidari
31	816	37.0	4639	1	DYHC_DROME	P37276 drosophila
32	814	36.9	4036	1	RRPL_DUGBV	Q66431 dugbe virus
33	814	36.9	4568	1	DYHC_CAEEL	Q19020 caenorhabdi
34	814	36.9	4684	1	PLE1_HUMAN	Q15149 homo sapien
35	813	36.9	4447	1	PKSK_BACSU	P40803 bacillus su
36	810	36.7	362	1	BIOB_SYNY3	P73538 synechocyst
37	808	36.6	3511	1	MY15_MOUSE	Q9qzz4 mus musculu
38	808	36.6	4544	1	LRP1_HUMAN	Q07954 homo sapien
39	807	36.6	4829	1	BIR6_HUMAN	Q9nr09 homo sapien
40	807	36.6	5217	1	HTS1_COCCA	Q01886 cochliobolu
41	806	36.5	4466	1	DYHC_TRIGR	P23098 tripneustes
42	805	36.5	4393	1	PGBM_HUMAN	P98160 homo sapien
43	805	36.5	4753	1	LRP_CAEEL	Q04833 caenorhabdi
44	803	36.4	4273	1	PKSM_BACSU	P40872 bacillus su
45	803	36.4	4344	1	DYHC_EMENI	P45444 emericella

ALIGNMENTS

```
RESULT   1
BIOB_ARATH
ID   BIOB_ARATH     STANDARD;      PRT;   378 AA.
AC   P54967;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   BIOTIN SYNTHASE (EC 2.8.1.6) (BIOTIN SYNTHETASE).
GN   BIO2 OR BIOB OR AT2G43360 OR T01024.10.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. LANDSBERG ERECTA;
RX   MEDLINE=96417082; PubMed=8819873;
RA   Weaver L.M., Yu F., Wurtele E.S., Nikolau B.J.;
RT   "Characterization of the cDNA and gene coding for the biotin synthase
RT   of Arabidopsis thaliana.";
RL   Plant Physiol. 110:1021-1028(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. COLUMBIA; TISSUE=Leaf;
RA   Patton D., Pacella M., Ward E.;
RL   Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. COLUMBIA; TISSUE=Leaf;
RX   MEDLINE=96307524; PubMed=8680961;
RA   Baldet P., Ruffet M.L.;
RT   "Biotin synthesis in higher plants: isolation of a cDNA encoding
RT   Arabidopsis thaliana bioB-gene product equivalent by functional
RT   complementation of a biotin auxotroph mutant bioB105 of Escherichia
RT   coli K12.";
RL   C. R. Acad. Sci., III, Sci. Vie 319:99-106(1996).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. COLUMBIA;
RX   MEDLINE=20083487; PubMed=10617197;
RA   Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA   Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
RA   Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
RA   Moffat K.S., Cronin L.A., Shen M., VanAken S.E., Umayam L.,
RA   Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
RA   Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
RA   Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
RA   Venter J.C.;
RT   "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RT   thaliana.";
RL   Nature 402:761-768(1999).
CC   -!- CATALYTIC ACTIVITY: DETHIOBIOTIN + (S) = BIOTIN.
CC   -!- PATHWAY: LAST STEP IN BIOTIN BIOSYNTHESIS PATHWAY.
CC   -!- SIMILARITY: BELONGS TO THE BIOTIN AND LIPOIC ACID SYNTHETASES
CC       FAMILY.
```

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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; U24147; AAA80226.1; -.
DR   EMBL; U31806; AAC49445.1; -.
DR   EMBL; L34413; AAB39953.1; -.
DR   EMBL; AC002335; AAB64312.1; -.
DR   InterPro; IPR002684; Biotin_synth.
DR   Pfam; PF01792; Biotin_synth; 1.
KW   Biotin biosynthesis; Iron-sulfur; Transferase.
FT   METAL        94     94       IRON-SULFUR (POTENTIAL).
FT   METAL        98     98       IRON-SULFUR (POTENTIAL).
FT   METAL       101    101       IRON-SULFUR (POTENTIAL).
SQ   SEQUENCE   378 AA;  41681 MW;  B102E477E7353762 CRC64;


  Query Match           89.7%;  Score 1979;  DB 1;  Length 378;
  Best Local Similarity  80.8%;  Pred. No. 5.9e-38;
  Matches  308;  Conservative   49;  Mismatches   10;  Indels   14;  Gaps    3;

Qy       4 MLLARN-LRSRLRPPLAAA-------AAFSSAAAEAERAIRDGPRNDWSRPEIQAVYDSP 55
           |:| |: :||:|||:::::       :::|:|:|||||:||:|||||||| ||::|||||
Db       1 MMLVRSVFRSQLRPSVSGGLQSASCYSSLSAASAEAERTIREGPRNDWSRDEIKSVYDSP 60

Qy      56 LLDLLFHGAQVHRNVHKFREVQQCTLLSIKTGGCSEDCSYCPQSSRYNTGLKAQKLMNKD 115
           |||||||||||||:||:|||||||||||||||||||||||||||||:||:|||:||:||
Db      61 LLDLLFHGAQVHRHVHNFREVQQCTLLSIKTGGCSEDCSYCPQSSRYSTGVKAQRLMSKD 120

Qy     116 AVLEAAKKAKAESGSTRFCMGAAWRETIGRKSNFNQILEYVKEIRGMGMEVCCTLGMIEKQ 175
           ||::|||||||:|||||||||||||:|||||:||:|||||:||||||||||||||||||||
Db     121 AVIDAAKKAKEAGSTRFCMGAAWRDTIGRKTNFSQILEYIKEIRGMGMEVCCTLGMIEKQ 180

Qy     176 QAEELKKAGLTAYNHNLDTSREYYPNIITTRSYDDRLQTLEHVREAGISICSGGIIGLGE 235
           || |||||||||||||||||||:||||||||||:|| |||:|||::|||||||||||||||
Db     181 QALELKKAGLTAYNHNLDTSREYYPNVITTRSYDDRLETLSHVRDAGINVCSGGIIGLGE 240

Qy     236 AEEDRVGLLHTLATLPTHPESVPINALVAVKGTPLEDQKPVEIWEMIRMIATARITMPKA 295
           |||||:||||||||||:||||||||||:||||||||||||||||||||:|||| ||||
Db     241 AEEDRIGLLHTLATLPSHPESVPINALLAVKGTPLEDQKPVEIWEMIRMIGTARIVMPKA 300

Qy     296 MVRLSAGRVRFSMPEQALCFLAGANSIFAGEKLLTTANNDFDADQAMFKILGLIPKAPSF 355
           |||||||||||||:|||||||||||||:|||||||:|||||||| ||| ||||||:|||
Db     301 MVRLSAGRVRFSMSEQALCFLAGANSIFTGEKLLTTPNNDFDADQLMFKTLGLIPKPPSF 360

Qy     356 GEEEVSAAAPAESERSEQAAS 376
           :|::      :|||  |: ||
Db     361 SEDD------SESENCEKVAS 375


RESULT   2
BIOB_SCHPO
ID   BIOB_SCHPO     STANDARD;      PRT;   363 AA.
AC   O59778; O60050;
DT   20-AUG-2001 (Rel. 40, Created)
DT   20-AUG-2001 (Rel. 40, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   BIOTIN SYNTHASE (EC 2.8.1.6) (BIOTIN SYNTHETASE).
GN   BIO2 OR SPCC320.01C OR SPCC1235.02.
OS   Schizosaccharomyces pombe (Fission yeast).
OC   Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC   Schizosaccharomycetales; Schizosaccharomycetaceae;
OC   Schizosaccharomyces.
OX   NCBI_TaxID=4896;
RN   [1]
RP   SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC   STRAIN=D18;
RX   MEDLINE=99456674; PubMed=1052584;
RA   Phalip V., Jeltsch J.M., Lemoine Y.;
RT   "Cloning of Schizosaccharomyces pombe bio2 by heterologous
RT   complementation of a Saccharomyces cerevisiae mutant.";
RL   Curr. Microbiol. 39:348-350(1999).
RN   [2]
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RC   STRAIN=972;
RA   Wood V., Rajandream M.A., Barrell B.G., Wedler H., Wambutt R.;
RL   Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
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CC   ----------------------------------------------------------------------
DR   EMBL; AJ224930; CAA12229.1; -.
DR   EMBL; AL022245; CAA18303.1; -.
DR   EMBL; AL031764; CAA21106.1; -.
DR   InterPro; IPR002684; Biotin_synth.
DR   Pfam; PF01792; Biotin_synth; 1.
KW   Biotin biosynthesis; Iron-sulfur; Transferase.
FT   METAL        69     69       IRON-SULFUR (POTENTIAL).
FT   METAL        73     73       IRON-SULFUR (POTENTIAL).
FT   METAL        76     76       IRON-SULFUR (POTENTIAL).
FT   CONFLICT     13     14       SS -> FF (IN REF. 1).
FT   CONFLICT     17     17       S -> F (IN REF. 1).
FT   CONFLICT    312    318       TTPAVSW -> LLLLFL (IN REF. 1).
SQ   SEQUENCE   363 AA;  40650 MW;  008E2EDF9901AEB1 CRC64;


  Query Match           62.1%;  Score 1369;  DB 1;  Length 363;
  Best Local Similarity  52.8%;  Pred. No. 5.3e-23;
  Matches  204;  Conservative   81;  Mismatches   65;  Indels   36;  Gaps    6;

Qy       5 LLARNLRSRLRPPLAAAAAFSSAAAEAERAIRDGP----RNDWSRPEIQAVYDSPLLDLL 60
           :::|::| ::|                     | ::    ||:|:| ||| :||:||:||:
Db       1 MFTRTIRQQIR-------------------RSSALSLVRNNWTREEIQKIYDTPLIDLI 40

Qy      61 FHGAQVHRNVHKFREVQQCTLLSIKTGGCSEDCSYCPQSSRYNTGLKAQKLMNKDAVLEA 120
           |::| :||: |  : |||||||||||||||:||| ||:||||||||:|| |||: | |||
Db      41 FRAASIHRKFHDPKKVQQCTLLSIKTGGCTEDCKYCAQSSRYNTGVKATKLMKIDEVLEK 100

Qy     121 AKKAKESGSTRFCMGAAWRETIGRKSNFNQILEYVKEIRGMGMEVCCTLGMIEKQQAEEL 180
           || ||  ||||||||:|||:  ||: :|::||| :||:|:|:|:|||| ||||:: ||| ||
Db     101 AKIAKAKGSTRFCMGSAWRDLNGRNRTFKNILEIIKEVRSMDMEVCVTLGMLNEQQAKEL 160

Qy     181 KKAGLTAYNHNLDTSREYYPNIITTRSYDDRLQTLEHVREAGISICSGGIIGLGEAEEDR 240
           | |||||||||||||||::||:||:||:|:::::| ||: :|||||:|||| :|| ||||
Db     161 KDAGLTAYNHNLDTSREYYSKIISTRTYDERLNTIDNLRKAGLKVCSGGILGLGEKKHDR 220

Qy     241 VGLLHTLATLPTHPESVPINALVAVKGTPLED--QKPVEIWEMIRMIATARITMPKAMVR 298
           |||:|:|||:|||||||||:| ||:: |||: |  :  : |    :| |||||| |||:::|
Db     221 VGLIHSLATMPTHPESVPFNLLVPIPGTPVGDAVKERLPIHPFLRSIATARICMPKTIIR 280

Qy     299 LSAGRVRFSMPEQALCFLAGANSIFAGEKLLTTANNDFDADQAMFKILGLIPKAPSF--- 355
           ::|||   | :|||| |:||||::|:|||:|||:   :|:|  :|   ||     ||
Db     281 FAAGRNTCSESEQALAFMAGANAVFTGEKMLTTPAVSWDSDSQLFYNWGLEGM-QSFEYG 339

Qy     356 ----GEEEVSAAAPAESERSEQAASM 377
               ||:   : :|   ||   ::|:
Db     340 TSTEGEDGTFTLPP--KERLAPSPSL 363
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